

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 4, 2005, 17:11:06 ; Search time 1431 Seconds

(Without alignments)
9973.393 Million cell updates/sec

Title: US-09-868-677-5

Perfect score: 2067 1 atgcctgcaccttcgacccct.....tgatcgacatttagatttt 2067

Sequence: 1 atgcctgcaccttcgacccct.....tgatcgacatttagatttt 2067

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7442561 seqs, 3452328358 residues 14885122

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
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- 16: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
- 20: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
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- 22: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
- 23: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
- 24: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
- 25: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
- 26: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	813.8	39.4	1380	US-10-385-802-17	Sequence 17, Appl
2	813.4	39.4	1377	US-10-385-802-7	Sequence 9, Appl
3	813.4	39.4	1377	US-10-385-802-9	Sequence 31, Appl
4	812.6	39.3	1389	US-10-385-802-31	Sequence 27, Appl
5	812.6	39.3	1470	US-10-385-802-29	Sequence 23, Appl
6	812.6	39.3	1470	US-10-385-802-27	Sequence 23, Appl
7	812.6	39.3	1947	US-10-385-802-23	Sequence 23, Appl

8	812.6	39.3	1998	US-10-385-802-25	Sequence 25, Appl
9	812.6	39.3	2094	US-10-385-802-47	Sequence 47, Appl
10	812.6	39.3	2118	US-10-385-802-21	Sequence 21, Appl
11	812.6	39.3	2181	US-10-385-802-19	Sequence 19, Appl
12	812.6	39.3	2652	US-10-385-802-11	Sequence 11, Appl
13	812.2	39.3	1377	US-10-385-802-45	Sequence 45, Appl
14	792.8	38.4	1589	US-10-385-802-45	Sequence 45, Appl
15	711.8	34.4	2003	US-10-809-790-3	Sequence 43, Appl
16	706.2	34.2	2003	US-10-809-790-3	Sequence 3, Appl
17	705.4	34.1	1359	US-09-773-877A-15	Sequence 15, Appl
18	705.4	34.1	1359	US-10-988-243-5	Sequence 5, Appl
19	705.4	34.1	1359	US-11-016-097-5	Sequence 5, Appl
20	705.4	34.1	1389	US-09-773-877A-17	Sequence 17, Appl
21	705.4	34.1	1389	US-10-988-243-7	Sequence 7, Appl
22	705.4	34.1	1389	US-11-016-097-7	Sequence 7, Appl
23	705.4	34.1	1574	US-09-773-877A-13	Sequence 13, Appl
24	705.4	34.1	1574	US-10-988-243-3	Sequence 3, Appl
25	705.4	34.1	1574	US-11-016-097-3	Sequence 3, Appl
26	705.4	34.1	1704	US-09-773-877A-11	Sequence 11, Appl
27	705.4	34.1	1704	US-09-773-877A-19	Sequence 19, Appl
28	705.4	34.1	1704	US-10-988-243-9	Sequence 9, Appl
29	705.4	34.1	1704	US-11-016-097-1	Sequence 1, Appl
30	705.4	34.1	1704	US-11-016-097-9	Sequence 9, Appl
31	705.4	34.1	1704	US-10-887-230-33	Sequence 33, Appl
32	705	34.1	1419	US-10-887-230-25	Sequence 25, Appl
33	705	34.1	1419	US-09-825-012-44	Sequence 44, Appl
34	702.2	34.0	2196	US-09-825-012-45	Sequence 45, Appl
35	702.2	34.0	2226	US-09-825-012-53	Sequence 53, Appl
36	702.2	34.0	2226	US-09-825-012-54	Sequence 54, Appl
37	702.2	34.0	2226	US-11-007-886-36	Sequence 36, Appl
38	700.2	33.9	1366	US-11-007-886-36	Sequence 36, Appl
39	700.2	33.9	1366	US-11-007-886-36	Sequence 37, Appl
40	700.2	33.9	1375	US-10-418-836-37	Sequence 37, Appl
41	700.2	33.9	1375	US-11-007-886-37	Sequence 37, Appl
42	700	33.9	7427	US-10-617-619-13	Sequence 13, Appl
43	700	33.9	7493	US-10-617-619-10	Sequence 10, Appl
44	699.4	33.8	4661	US-09-897-006-10	Sequence 10, Appl
45	699.4	33.8	4661	US-09-897-511A-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-10-385-802-17
Sequence 17, Application US/10385802
GENERAL INFORMATION:
APPLICANT: Dhanabai, Mohanraj
APPLICANT: Laroche, William J.
APPLICANT: Lichtenstein, Henri
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND AMINO ACID SEQUENCES OF
FILE REFERENCE: 15966-517UB
CURRENT APPLICATION NUMBER: US/10/385,802
PRIOR FILING DATE: 2003-03-11
PRIOR APPLICATION NUMBER: 60/363,266
NUMBER OF SEQ ID NOS: 77
SOFTWARE: Cursesqlist version 0.1
SEQ ID NO 17
LENGTH: 1380
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1377)
US-10-385-802-17
Query Match 39.4% Score 813.8; DB 17; Length 1380;
Best Local Similarity 76.8%; Pred. No. 2.7e-219;
Matches 1040; Conservative 0; Mismatches 297; Indels 18; Gaps 3;

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OM protein - protein search, using SW model

Run on: October 4, 2005, 17:12:22 ; Search time 169 Seconds
(without alignments)
1689.940 Million cell updates/sec

Title: US-09-868-677-6
Perfect score: 3834
Sequence: 1 MSALLILVGAIVARDCAD.....YFKGPSYSLSRTTMMIRPLD 688

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1846076 seqs, 415116000 residues
Total number of hits satisfying chosen parameters: 1846076

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2507.5	65.7	702	US-11-035-599-52	Sequence 52, Appl
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3	2116.5	55.5	702	US-11-035-599-53	Sequence 53, Appl
4	2105.5	55.2	730	US-11-035-599-31	Sequence 31, Appl
5	1757	46.1	462	US-10-385-802-46	Sequence 46, Appl
6	1757	46.1	697	US-10-385-802-48	Sequence 48, Appl
7	1745	45.8	459	US-10-385-802-12	Sequence 12, Appl
8	1743.5	45.7	489	US-10-385-802-44	Sequence 44, Appl
9	1742	45.7	459	US-10-385-802-8	Sequence 8, Appl
10	1742	45.7	459	US-10-385-802-18	Sequence 18, Appl
11	1737	45.5	458	US-10-385-802-10	Sequence 10, Appl

12	1725.5	45.2	526	US-10-385-802-52	Sequence 52, Appl
13	1720.5	45.1	462	US-10-385-802-32	Sequence 32, Appl
14	1720.5	45.1	489	US-10-385-802-10	Sequence 30, Appl
15	1720.5	45.1	588	US-10-385-802-28	Sequence 28, Appl
16	1720.5	45.1	648	US-10-385-802-24	Sequence 24, Appl
17	1720.5	45.1	665	US-10-385-802-26	Sequence 26, Appl
18	1720.5	45.1	705	US-10-385-802-22	Sequence 22, Appl
19	1720.5	45.1	726	US-10-385-802-20	Sequence 20, Appl
20	1720.5	45.1	883	US-10-385-802-2	Sequence 2, Appl
21	1694	44.4	588	US-10-385-802-40	Sequence 40, Appl
22	1689	44.3	588	US-10-385-802-42	Sequence 42, Appl
23	1684	44.2	588	US-10-385-802-38	Sequence 38, Appl
24	1664	43.6	665	US-10-385-802-16	Sequence 16, Appl
25	1655.5	43.4	665	US-10-385-802-18	Sequence 18, Appl
26	1635.5	42.9	705	US-10-385-802-34	Sequence 34, Appl
27	1631	42.6	465	US-10-887-230-43	Sequence 43, Appl
28	1311	34.0	485	US-10-887-230-26	Sequence 26, Appl
29	1297.5	34.0	631	US-10-120-1988-2	Sequence 2, Appl
30	1295.5	34.0	659	US-10-809-790-4	Sequence 4, Appl
31	1295.5	34.0	734	US-11-035-599-50	Sequence 50, Appl
32	1295.5	34.0	949	US-10-232-838-19	Sequence 19, Appl
33	1284	33.9	641	US-10-723-003-46	Sequence 46, Appl
34	1282	33.9	452	US-09-773-877A-16	Sequence 16, Appl
35	1292	33.9	452	US-10-988-243-6	Sequence 6, Appl
36	1292	33.9	452	US-11-016-097-6	Sequence 6, Appl
37	1292	33.9	557	US-09-773-877A-14	Sequence 14, Appl
38	1292	33.9	557	US-10-988-243-4	Sequence 4, Appl
39	1292	33.9	557	US-11-016-097-4	Sequence 4, Appl
40	1292	33.9	761	US-11-035-599-29	Sequence 29, Appl
41	1292	33.9	762	US-11-035-599-28	Sequence 28, Appl
42	1291.5	33.9	731	US-11-035-599-51	Sequence 51, Appl
43	1290.5	33.8	462	US-09-773-877A-18	Sequence 18, Appl
44	1290.5	33.8	462	US-10-988-243-8	Sequence 8, Appl
45	1290.5	33.8	462	US-11-016-097-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-11-035-599-52
Sequence 52, Application US/11035599
Publication No. US20050158829A1
GENERAL INFORMATION:
APPLICANT: Fandl, James
APPLICANT: Chen, Gang
APPLICANT: Papadopoulos, Nicholas
APPLICANT: Aldrich, Thomas P.
TITLE OF INVENTION: Fusion Polypeptides Capable of
FILE REFERENCE: 1080A
CURRENT APPLICATION NUMBER: US/11/035, 599
CURRENT FILING DATE: 2005-01-14
PRIOR APPLICATION NUMBER: 60/536, 968
PRIOR FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 52
LENGTH: 702
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-11-035-599-52

Query Match 65.7%, Score 2507.5, DB 20, Length 702;
Best Local Similarity 85.2%, Pred. NO. 1.6e-178;
Matches 471; Conservative 14; Mismatches 27; Indels 41; Gaps 7;
QY 145 GKSSLLIHGADFSTKXDNDNCMKCALMTGGMWFDACPSNINGMFYAGONG-KL 203
DB 181 GKSQLLVYGA---TNLADG-----VPSRPSGS--GSGTQYSLKI 215

OM nucleic - nucleic search, using sw model

Run on: October 4, 2005, 17:11:06 ; Search time 359 Seconds
(without alignments)
9421.125 Million cell updates/sec

Title: US-09-868-677-5
Perfect score: 2067
Sequence: 1 atgcctgaccttcgaccccttgcattgcaccccttcatttc 2067

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
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4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PTCTS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	705.4	34.1	1359	US-09-773-877B-15	Sequence 15, Appl
2	705.4	34.1	1389	US-09-773-877B-17	Sequence 17, Appl
3	705.4	34.1	1674	US-09-773-877B-13	Sequence 13, Appl
4	705.4	34.1	1704	US-09-773-877B-11	Sequence 11, Appl
5	705.4	34.1	1704	US-09-773-877B-19	Sequence 19, Appl
6	698.6	33.8	9209	US-08-149-099C-3	Sequence 3, Appl
7	698.6	33.8	9209	US-08-476-275-2	Sequence 2, Appl
8	698.6	33.8	9209	US-08-478-967A-3	Sequence 3, Appl
9	698.6	33.8	9209	US-08-475-815B-3	Sequence 3, Appl
10	698.6	33.8	9209	US-08-475-815-2	Sequence 2, Appl
11	698.6	33.8	18986	US-08-819-866-2	Sequence 2, Appl
12	698.6	33.8	18986	US-09-023-715-2	Sequence 2, Appl
13	698.6	33.8	18986	US-09-343-485A-2	Sequence 2, Appl
14	698.6	33.8	19040	US-09-343-485A-3	Sequence 3, Appl
15	697.4	33.7	1019	US-09-178-869-1	Sequence 1, Appl
16	697.4	33.7	1019	US-09-761-413-1	Sequence 1, Appl
17	697.4	33.7	1182	US-09-180-100-18	Sequence 18, Appl
18	697	33.7	1080	US-09-180-100-14	Sequence 14, Appl
19	697	33.7	1272	US-09-038-175-5	Sequence 5, Appl
20	697	33.7	1272	US-08-030-175-6	Sequence 6, Appl
21	696.8	33.7	1458	US-08-030-175-7	Sequence 7, Appl
22	696.8	33.7	1458	US-08-030-175-5	Sequence 5, Appl
23	696.8	33.7	1458	US-08-030-175-5	Sequence 5, Appl
24	696.8	33.7	1599	US-09-023-655-1120	Sequence 1120, Ap
25	696.8	33.7	1617	US-08-378-939-9	Sequence 9, Appl
26	696.6	33.7	1720	US-09-746-359A-52	Sequence 52, Appl
27	696.4	33.7	1428	US-08-488-376-19	Sequence 19, Appl

28	696.4	33.7	1428	US-08-634-223-19	Sequence 19, Appl
29	696.4	33.7	1428	US-08-634-224-19	Sequence 19, Appl
30	696.4	33.7	1428	US-08-634-400-19	Sequence 19, Appl
31	696.4	33.7	1428	US-08-635-878-19	Sequence 19, Appl
32	696.4	33.7	1428	US-08-770-057-19	Sequence 19, Appl
33	696.4	33.7	1428	US-09-335-697B-19	Sequence 19, Appl
34	696.4	33.7	1428	US-09-335-697B-19	Sequence 19, Appl
35	696.4	33.7	1428	US-09-740-002-19	Sequence 19, Appl
36	696.4	33.7	1431	US-08-487-550-3	Sequence 3, Appl
37	696.4	33.7	1431	US-08-487-550-11	Sequence 11, Appl
38	696.4	33.7	1431	US-09-526-098-3	Sequence 3, Appl
39	696.4	33.7	1431	US-09-526-098-11	Sequence 11, Appl
40	696.4	33.7	1431	US-09-383-916-3	Sequence 3, Appl
41	696.4	33.7	1431	US-09-383-916-11	Sequence 11, Appl
42	696.4	33.7	1437	US-08-487-550-7	Sequence 7, Appl
43	696.4	33.7	1437	US-09-526-098-7	Sequence 7, Appl
44	696.4	33.7	1437	US-09-383-916-7	Sequence 7, Appl
45	696.4	33.7	1494	US-09-499-846-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-773-877B-15
Sequence 15, Application US/09773877B
Patent No. 683349
GENERAL INFORMATION:
APPLICANT: Xia, Yu-Ping et al.
TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
FILE REFERENCE: REG 710b
CURRENT APPLICATION NUMBER: US/09/773, 877B
CURRENT FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.0
SEQ ID NO 15
LENGTH: 1359
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1359)
US-09-773-877B-15

Query Match 34.1%, Score 705.4; DB 4; Length 1359;
Best Local Similarity 99.9%; Pred. No. 3.6e-184;
Matches 706; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB	652	GGCCCGGCGAGCCCAATCTTGACAAACTACACATGCCACCGTCCAGCACTT	711
QY	751	GAACTCCCTGGGGGACCGTCACTCTTCCCTCCCAAAACCGAGACACCTCATG	810
DB	712	GAACTCCCTGGGGGACCGTCACTCTTCCCTCCCAAAACCGAGACACCTCATG	771
QY	811	ATCTCCCGGAGCCCTGAGTGCATCGGTGTGTGACGTAAGCAAGACCTTGTAG	870
DB	772	ATCTCCCGGAGCCCTGAGTGCATCGGTGTGTGACGTAAGCAAGACCTTGTAG	831
QY	871	GTCAGTTCAACTGTGACGTGACGCGGTGAGGTGATTAATGCCAAGACCGCGG	930
DB	832	GTCAGTTCAACTGTGACGTGACGCGGTGAGGTGATTAATGCCAAGACCGCGG	891
QY	931	GAGAGGAGTCAACACACACGTAACCGTGTGTGACGCTTCCACCGTCCACAGAC	990
DB	892	GAGAGGAGTCAACACACACGTAACCGTGTGTGACGCTTCCACCGTCCACAGAC	951
QY	991	TGGCTGATGCAAGAGTCAAGTCAAGTCTCCAAAGAGCTTCCAGCCCTATC	1050
DB	952	TGGCTGATGCAAGAGTCAAGTCAAGTCTCCAAAGAGCTTCCAGCCCTATC	1011

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2005, 17:12:22 ; Search time 43 Seconds
(without alignments)
1194.385 Million cell updates/sec

Title: US-09-868-677-6

Perfect score: 3814
Sequence: 1 MSALLILVGAAVARDCAD.....YFKGFSYSLRSTTMIRPD 688

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 7464964 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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4: /cgn2_6/prodata/1/iaa/6C_COMB.pep:*
5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1292	33.9	452	4	US-09-773-877B-16 Sequence 16, Appl
2	1292	33.9	557	4	US-09-773-877B-14 Sequence 14, Appl
3	1290.5	33.8	462	4	US-09-773-877B-18 Sequence 18, Appl
4	1290.5	33.8	567	4	US-09-773-877B-12 Sequence 12, Appl
5	1290.5	33.8	567	4	US-09-773-877B-20 Sequence 20, Appl
6	1282	33.6	711	3	US-09-485-737B-90 Sequence 90, Appl
7	1282	33.6	711	4	US-10-071-485-90 Sequence 90, Appl
8	1280	33.6	476	3	US-08-487-550-4 Sequence 4, Appl
9	1280	33.6	476	4	US-09-526-098-4 Sequence 4, Appl
10	1280	33.6	476	4	US-09-383-916-4 Sequence 4, Appl
11	1276.5	33.5	622	4	US-09-499-846-2 Sequence 2, Appl
12	1275.5	33.4	911	2	US-08-484-438-10 Sequence 10, Appl
13	1275	33.4	859	4	US-09-313-942-7 Sequence 7, Appl
14	1274.5	33.4	497	4	US-09-499-846-6 Sequence 6, Appl
15	1274.5	33.4	525	2	US-09-499-846-4 Sequence 4, Appl
16	1272	33.4	396	2	US-08-784-512-3 Sequence 3, Appl
17	1272	33.4	396	3	US-09-176-228-3 Sequence 3, Appl
18	1272	33.4	450	4	US-09-996-288-216 Sequence 216, Appl
19	1272	33.4	450	4	US-09-996-288-218 Sequence 218, Appl
20	1272	33.4	450	4	US-09-996-288-250 Sequence 250, Appl
21	1272	33.4	476	3	US-08-487-550-12 Sequence 12, Appl
22	1272	33.4	476	4	US-09-526-098-12 Sequence 12, Appl
23	1272	33.4	476	4	US-09-383-916-12 Sequence 12, Appl
24	1270	33.3	977	4	US-09-590-656-1 Sequence 1, Appl
25	1270	33.3	977	4	US-09-733-764-1 Sequence 11, Appl
26	1269	33.3	437	5	PCT-US96-10043-11 Sequence 8, Appl
27	1269	33.3	592	4	US-09-313-942-8 Sequence 8, Appl

28	1268.5	33.3	277	4	US-09-428-082B-22 Sequence 22, Appl
29	1268	33.2	450	4	US-09-996-288-228 Sequence 228, Appl
30	1268	33.2	450	4	US-09-996-288-248 Sequence 248, Appl
31	1267.5	33.2	424	5	PCT-US95-03866-12 Sequence 12, Appl
32	1267.5	33.2	424	5	PCT-US95-03866-14 Sequence 14, Appl
33	1267	33.2	442	4	US-08-472-888A-7 Sequence 7, Appl
34	1267	33.2	442	5	PCT-US96-10043-9 Sequence 9, Appl
35	1266	33.2	475	4	US-09-740-002-27 Sequence 27, Appl
36	1265.5	33.2	450	4	US-09-996-288-208 Sequence 208, Appl
37	1265.5	33.2	451	4	US-09-996-288-230 Sequence 230, Appl
38	1265.5	33.2	951	4	US-09-313-942-9 Sequence 9, Appl
39	1265	33.2	253	4	US-09-428-082B-16 Sequence 16, Appl
40	1265	33.2	450	4	US-09-996-288-222 Sequence 222, Appl
41	1265	33.2	450	4	US-09-996-288-224 Sequence 224, Appl
42	1265	33.2	452	3	US-09-027-448-71 Sequence 71, Appl
43	1265	33.2	452	3	US-09-026-985-71 Sequence 71, Appl
44	1265	33.2	452	4	US-09-121-952A-71 Sequence 71, Appl
45	1265	33.2	452	4	US-09-234-340A-71 Sequence 71, Appl

ALIGNMENTS

RESULT 1
US-09-773-877B-16
Sequence 16, Application US/09773877B
Patent No. 683349
GENERAL INFORMATION:
APPLICANT: Xia, Yu-Ping et al.
TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
FILE REFERENCE: REG 710b
CURRENT APPLICATION NUMBER: US/09/773,877B
CURRENT FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patent version 3.0
SEQ ID NO 16
LENGTH: 452
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Flt1(2-3 deltab)-Fc
US-09-773-877B-16

Query Match 33.9%; Score 1292; DB 4; Length 452;
Best Local Similarity 76.4%; Pred. No. 2.5e-107;
Matches 259; Conservative 12; Mismatches 34; Indels 34; Gaps 9;

QY	137	LGHTGTAGKQSSLIHGADPSTKADNDNCCKCAL-----MLTGWMP-DACGSPNIN- 190
DB	138	LGHT-----LVL-----NCYATPLTRVQMT--WSYDEIDQSNSHA 174
QY	191	GMFY---TAGQNHGKLANGI-KWYFKGSPYSLSRSTMMIRPLDPGCPKSCDKHTCP 246
DB	175	NIFYSVLTIDKQNDKGLYTCRVASGSPFSKVSNTSVIYD-KAGPGPKSCDKHTCP 233
QY	247	CPAPILGGPSVFLPPPKXTLMSRTPEVYCVVVDVSHEDPEYKFWYDGVENNAK 306
DB	234	CPAPILGGPSVFLPPPKXTLMSRTPEVYCVVVDVSHEDPEYKFWYDGVENNAK 293
QY	307	TPREBOVNSTRVVSVTLVHODMLNGEKYCKVSNALPAPIKTTISKAGOPREPOV 366
DB	294	TPREBOVNSTRVVSVTLVHODMLNGEKYCKVSNALPAPIKTTISKAGOPREPOV 353
QY	367	YTLPSRDELITNGVSLTCLVKGFPSPDIAMWESNGOPENNKKTPPLVDSGSPFLYS 426
DB	354	YTLPSRDELITNGVSLTCLVKGFPSPDIAMWESNGOPENNKKTPPLVDSGSPFLYS 413
QY	427	KLTVDKSRMOQGNVSCVMEHAIHNHYTKSLISPSGK 465
DB	414	KLTVDKSRMOQGNVSCVMEHAIHNHYTKSLISPSGK 452

RESULT 2